

CRYPTIC GENETIC DIVERSITY IN THE GENUS *MESOPODOPSIS* (CRUSTACEA, MYSIDACEA)

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Genetic biodiversity is dynamic, species and their environment undergo continuously evolutionary changes. The start of these evolutionary changes always takes place at the population level. Genetic (allele) variation is caused by mutation, intraspecific and interspecific recombination. The survival of these new alleles is determined by selection, genetic drift and gene flow. Since molecular techniques have become more accessible in diversity research, it became clear that genetic biodiversity is strongly underestimated. The existence of cryptic genetic diversity has been revealed in numerous marine taxa (Knowlton, 2000). Next to the dispersal potential of a species other factors (such as hydrodynamic currents, dispersal limitation by larval behaviour, selection by local adaptation and historical barriers) have an important influence on population genetic divergence.

Mesopodopsis slabberi is one of the most common mysids along the European coasts. The lack of pelagic larvae and the broad geographic distribution of the species, makes it an interesting model organism for evolutionary research on patterns of cryptic speciation (Remerie *et al.*, 2006). In the present study, the degree and causes of cryptic speciation within the species *M. slabberi* were further investigated. By analysing populations of different habitats (lagoons, surf zones, estuaria, marshes) and by focusing on the Atlantic–Mediterranean transition zone, we tried to create a better vision about the contemporary and historical phenomena and the ecological background behind the observed genetic diversity. The phylogeographic patterns among populations were analysed by means of DNA sequencing of a fragment of the mitochondrial cytochrome c oxidase subunit 1 (COI) and the 16S ribosomal RNA genes. We concluded that a high level of cryptic speciation was present within *Mesopodopsis slabberi*, with at least 6 cryptic lineages (2 Atlantic, 3 Mediterranean and 1 Black Sea). These levels of cryptic diversity are discussed in a contemporary and historical framework.

References

- Knowlton N. 2000. Molecular genetic analysis of species boundaries in the sea. *Hydrobiologia* 420:73-90.
- Remerie T., T. Bourgois, D. Peelaers, A. Vierstraete, J. Vanfleteren, and A. Vanreusel. 2006. Phylogeographic patterns within the mysid *Mesopodopsis slabberi* (Crustacea, Mysida): evidence for high molecular diversity and cryptic speciation. *Mar. Biol.* 149:465-481.